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GENETIC DIVERGENCE IN HORSEGRAM (*MACROTYLOMA UNIFLORUM* (Lam) Verdc.)

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Horsegram, a traditionally very important pulse of South India, has been an important pulse of U.P. hills since time immemorial. To strengthen the ongoing breeding programme, several horsegram accessions were procured from different sources.

Fourty horsegram genotypes procured from National Bureau of Plant Genetic Resources (NBPGR), Regional Stations Bhowali, Akola and Shimla, University of Agricultural Sciences (UAS), Bangalore and four local collections were sown in a randomized complete block design with three replications. Data were recorded on days to initiation of twines (TI), 50% flowering (FL), maturity (MT), plant dry weight (g) six weeks after sowing (DW), plant height (PH), pod length (PL) in cm, number of pods per plant (PP), number of grains per pod (GP), 100-grain weight (GW) and grain yield per plant (YP) in grams. Each plot consisted of a row of 1.75 m length and the row to row spacing was maintained at 0.45 m. Data were subjected to analysis as per Mahalanobis (1936) and Rao (1952).

Studying variation among newly procured germplasm lines to generate information on the nature and magnitude of genetic divergence is quite logical. This helps breeders to choose diverse parents for purposeful hybridization (Arunachalam, 1981; Samsuddin, 1985). The significant treatment mean squares indicated potent variability among the genotypes studied. Based on D^2 values for all possible 780 cultivar pairs, the 40 cultivars were grouped into six clusters. This indicates the presence of a large amount of diversity among the

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Table 1. Distribution of horsegram genotypes among different clusters

Cluster	No. of Genotypes	Genotypes
I	23	Arka local, Macintosh, Sapatu local, Sundar nagar local, P- 2056, NIC-2921, Bilaspur local, HPK-2, VLG-1, C-6-3-4, P-1610, Raigarh local, NIC-2913, P-1648, NIC-762, P-1192, S-67/14, PHG-20, Mandi local, P2030, NIC-2659, KN-825, P-1955
II	6	BU & 7-1, D-6-3-4, PLKV-38, DO-377, BDT-89-5, P-1659.
III	7	VLG-2, P-192, P-1910, Almora local-2, NIC-7321, NIC- 2757, R1711
IV	2	Tumkur local, Almora local-1
V	1	AU-6-4-2
VI	1	P-1668

Table 2. Intra and inter cluster distance (D^2) among six clusters in horsegram

Cluster	I	II	III	IV	V	VI
I	145.4	29.2	24.6	43.6	49.9	34.9
II		53.4	44.4	38.4	60.9	38.7
III			57.8	52.8	79.6	52.0
IV				8.6	66.2	57.6
V					0.0	116.0
VI						0.0

genotypes for all the traits studied (Table 1). Cluster 1 was the biggest with 23 genotypes, cluster II had six, cluster III had seven, IV had two and clusters V and VI had one genotype each. The intracluster distance ranged from 0.0 (clusters V and VI) to 145.4 (cluster I). The cluster I comprised of a big heterogeneous group of 23 genotypes. The maximum intercluster distance of 116.0 was recorded between clusters V and VI, followed by 79.6 between V and III suggesting wide diversity among these groups. On the other hand the minimum distance (24.6) between clusters I and III indicated their close relationship.

Based on cluster means, the important clusters are : III for pods per plant, I and VI for grain weight, I, III, IV and V for number of grains per pod, and III, V and I for grain yield. Crosses involving parents from divergent

Table 3. Means (M), standard errors (SE) and coefficient of variation (CV) for different characters in the six clusters

Character/ Cluster		TI	FL	MT	DW	PH	PL	PP	GP	GW	YP
I	M	45.3	72.9	123.3	6.7	82.9	4.7	29.6	5.8	3.2	3.4
	SE	0.7	0.3	0.6	0.2	6.3	0.01	1.2	0.01	0.1	0.3
	CV	7.8	1.9	2.5	17.0	36.6	5.1	18.8	5.7	13.7	36.3
II	M	47.3	73.9	120.2	7.0	92.5	4.5	15.6	4.9	2.8	0.1
	SE	0.4	1.1	1.8	1.1	6.8	0.1	1.2	0.2	0.1	0.2
	CV	2.3	3.8	3.7	38.8	18.1	7.5	42.2	8.4	9.2	62.5
III	M	47.2	72.5	117.2	7.8	83.4	4.5	49.7	5.7	3.0	3.7
	SE	1.4	0.4	3.4	0.4	3.0	0.1	4.4	0.2	0.1	0.4
	CV	6.7	1.5	7.7	13.8	9.5	5.4	23.3	8.9	11.3	28.8
IV	M	44.5	83.3	123.5	7.8	96.0	4.5	20.3	5.6	2.3	1.6
	SE	0.5	0.0	0.8	0.8	11.7	0.1	2.0	0.5	0.5	0.4
	CV	1.6	0.0	0.9	14.5	17.3	3.1	13.9	12.6	30.7	31.9
V	M	49.0	74.3	154.3	5.6	83.3	4.9	22.3	5.5	2.5	3.6
VI	M	36.7	72.3	111.3	8.6	79.0	4.1	13.3	5.3	3.3	0.7

clusters are expected to manifest maximum heterosis and also wide variability in subsequent segregating generations. The clusters comprising only one genotype with specific traits could also be exploited in a hybridization programme. Thus, crosses between the genotypes of cluster III and those of clusters I and V are expected to exhibit high heterosis and are also likely to produce new recombinants with desired traits.

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